

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994; 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

9 Wed Aug 20 09:54:07 1997; MasPar time 12.22 Seconds 659.595 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-469-637A-2 (22-401) from US08469637A.pep (2 of 2) 2861 1 ETFPPKYLHYDEETSHQLLC......OKLFLEMIGNQVQSVKISCL 380

Scoring table: PAM 150 Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.034; Variance 81.732; scale 0.588

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4 4 5 4	43	42	4.1	40	39	38	37	36	ა 5	34	ω ω	32	31	30	29	28	27	26	25	24	23
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PGBM_MOUSE	MYSC_CAEEL	KAB7_YEAST	XCPE_XENLA	SYV_YEAST	PR31_YEAST	PHOR_SHIDY	YAQ5_SCHPO	DESP_HUMAN	YG3C_YEAST	GFA1_CANAL	LMA1_MOUSE		D2_DICDI	YIH9_YEAST	VA53_VACCV	VA53_VACCC	FASA_HUMAN	CD27_MOUSE	FASA_MOUSE	6	41BB_HUMAN
BASEMENT MEMBRANE-SPE DYNEIN HEAVY CHAIN, C	MYOSIN HEAVY CHAIN C	PROBABLE SERINE/THREO	CHROMOSOME ASSEMBLY P	VALYL-TRNA SYNTHETASE	PRE-MRNA SPLICING FAC	PHOSPHATE REGULON SEN	PUTATIVE TRANSLATIONA	DESMOPLAKIN I AND II	HYPOTHETICAL 128.8 KD	GLUCOSAMINE FRUCTOSE	LAMININ ALPHA-1 CHAIN	VON WILLEBRAND FACTOR	CAMP-REGULATED D2 PRO	HYPOTHETICAL 41.6 KD	PROTEIN A53.	C I	FASL RECEPTOR PRECURS	CD27L RECEPTOR PRECUR	FASL RECEPTOR PRECURS	OX40L RECEPTOR PRECUR	4-1BB LIGAND RECEPTOR
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ALIGNMENTS

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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

EMBL: M32315; G189186; -.

EMBL: M35857; G339752; -.

EMBL: M35857; G339758; -.

EMBL: M35994; G339758; -.

PIR: A35007; A36007.

PIR: A36007; A36007.

PIR: A36007; A36075.
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                   TNR2_MOUSE STANDARD: PRT: 474 AA. P25119: 01-MAY-1992 (REL. 22, CREATED) 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TIMER2 OR TIMER-2.
    SDW
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PIR; A23666;
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J. FUNCTION: RECEPTOR FOR THE AFFINITY FOR TWA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TWE-BETA.

-I- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
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RECEPTOR; TRANSMEMBRANE; GLY
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  MUSCULUS (MOUSE)
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BY SIMILARITY
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R -> M (IN

A -> T (IN
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CYTOPLASMIC (POTENTIAL)
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d. No. 6.30e-63;
Mismatches 59;
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NI) H
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N REF. 1).
N REF. 3).
N CRC32;
                                        (TNF-R2)
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Best Local
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01-MAY-1992 (RE)
01-MAY-1992 (RE)
01-JUN-1994 (RE)
CD40L RECEPTOR 1
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  SAPIENS (HUMAN).
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                                                         REL. 22, 0
REL. 22, 1
REL. 29, 1
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SEQUENCE FROM N.A.
MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A.
WONG G.H., CHEM E.Y., GC
PROC. NATL. ACAD. SCI. (
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HSSP; P19438; 1TUR_NGER.
PROSITE; P500652; TNFR_NGER.
PROSITE; P500652; GLYCOPROTEIN; REPEAT; SIGNAL.
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-I- FUNCTION: RECEPTOR FOR TNF-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 91246168.
GOODWIN R.G., ANDERSON
GOODELAND N.G., JENKINS
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!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                tkggnrvcaceagrycalkthsgscrqcmrlskcgpgfgvassrapngnvlckacapgtf 171 : :|: | :| | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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Pred. No. 3.
21; Mismatc
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4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
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TNFR-CYS 4.
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D.V.;
88:2830-2834(1991)
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3.56e-56;
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                                                                                                                 189
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STANDARD;

PRT;

CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT

(B-CELL

SURFACE

ANTIGEN CD40) (BP50) (CDW40)

UPDATE!

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Query Match
Best Local S
Matches 5
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CARBOHYD
SEQUENCE
SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE; 93094586.
GRIMALDI J.C., TORRES R., KC
                                                                                                                                                                                                                                                                  01-AUG-1992 (REL. 23, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAMENKOVIC I., CLARK E.A., SEED B.;
EMBO J. 8:1403-1410(1989).

-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD401-
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.

-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH
                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                            CD40_MOUSE
P27512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA;
EUTHERIA; F
                                                                        SUBMITTED (SEP-1996)
                                                                                     STRAIN-BALB/C;
TORRES R.M.;
                                                                                                                  REVISIONS
                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 92105763.
TORRES R.M., CLARK E.A.;
J. IMMUNOL. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR: S04460; S04460.
MIM: 109535; -.
PROSITE: PS00652; INFR_NGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89356608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECEPTOR; B-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-L--YCSPVCKELQYVKQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 cslcqpqqklvsdctefteteclpcgesefldtwnrethchqhkycdpn-lglr-vqqkg
                                                                                                                                                                                                                                                                                                                                                                                                SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRTHNRVCECKEGRY-L-EI-EFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tsetdtictceegwhctseacescvlhrscspgfgvkgiatgvsdticepcpvgffsnvs 155
                                                                                                                                                                                                                                                                                                                                                                                                                         safekchpwtscetkdlvvqqagtnktdvvcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X60592; G29851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
56; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIMATES.
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larity 36.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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                                                                        EMBL/GENBANK/DDBJ
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:
     KOZAK C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
4 X THER-CYS.
THER-CYS 1.
THER-CYS 2.
THER-CYS 3.
THER-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 303; DB 2; Le
Pred. No. 2.64e-40;
21; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
3B284411 CRC32;
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EXTRACELLULAR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                         289
                                                                                                                                                                                                                                                                                                                                                                                                186
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       CHANG
                                                                                                                                                                                                                                                                                                                                         A
                                                                         DATA BANKS
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       CLARK E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                             MAMMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      154
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  THE RESULT
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Best Local S
Matches 5
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EMBL; M94126; G192526; --
EMBL; M94129; G192526; JOINED.
EMBL; M94128; G192526; JOINED.
EMBL; M94127; G192526; JOINED.
EMBL; M94127; G192526; JOINED.
PIR; A46476; A46476.
                            PROSITE; I
RECEPTOR;
SIGNAL
                                                                                                                                                                                                                                                                                                                         01-APR-1993
01-APR-1993
01-FEB-1994
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SEQUENCE
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REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                  -!- FUNCTION: BINDS TO TWF-ALPHA AND BETA. PROBABLY PREVENTS INF:
REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
ANTIVIRAL EFFECTS OF THE CYTOKINE.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; M95181; G332310; -.
EMBL; A23729; E199442; -.
EMBL; A23729; E199442; -.
                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 91335768.
UPTON C., MACEN J.L., SCHR
VIROLOGY 184:370-382(1991)
                                                                                                                                                                                                                                                                 MYXOMA VIRUS (STRAIN LAUSANNE).
VIRIDAE; DS-DNA ENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                         01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECUR
                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                VT2_MYXVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. IMMUNOL.
                                                                                                                                                                                                                                                       VIRIDAE; DS-DNA
LEPORIPOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                     P29825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                         155 SSKAPCRKHINCSVFGLLLTQKGNATHDNICS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKELQYVKQEC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRTHNRVCECKEGRY-L--EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P19438; 1TNR.
                                                         P19438; ITNR.
PE; PS00652; TNFR_NGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 10.3%;
Similarity 38.8%;
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00652;
    ; GLYCOPROTEIN;
1 16
17 326
27 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCKAYNE D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149:3921-3926(1992).
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289
193
215
289
187
60
103
1144
187
153
32111
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                                                                                                                                                                                              SCHREIBER M., MCFADDEN
  ; REPEAT; SIGNAL.
POTENTIAL.
PROTEIN T2.
4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 294; DB 2; L
Pred. No. 2.31e-38;
20; Mismatches 65;
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TNFR-CYS 3.
TNFR-CYS 4.
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CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL)
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TNFR-CYS 1.
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                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                     POXVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                326
                                                                                                                                                                                                                                                                                                            PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC32
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                                                                                                                                                                                                                                                                     CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 289
                                                                                                                                                                                                                                                                                                              (PROTEIN T2).
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Best Local
REPEAT
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DOMAIN
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REPEAT
REPEAT
CARBOHYD
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                      EMBL; U29173; G881621;
EMBL; L38423; G600223;
EMBL; U30798; G1061327;
                                                                                                                                                                                                                                                                                                                                                                                                   GENOMICS 30:312-319(1995).
-!- FUNCTION: RECEPTOR FOR IMMUNE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 96163885.
NAKAMURA T., TASHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAN-CVB: TISSUE-LUNG;
FORCE W.R., WILLIAMS-ABBOTT L.,
WARE C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNRC_MOUSE
                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (JUN-1995) TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sstetctssfnyisvefnl 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctscppgsyasrlcgpgsdtvcspcknetftastnhapacvscrgrctghlsesgscdkt 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rdrvcdcsagnycllkgqegcricapktkcpagygvs-ghtrtgdvlctkcprytysdav 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 47; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105
148
148
181
181
205
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.4%;
larity 33.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K., NAZAREA M., NAKANO T., SASAYAMA
                                                                                                                                                                                                                                                                                                                                                                                                                      FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                  GLYCOPROTEIN; REPEAT; POTENTIAL.
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Pred. No. 5.03e-33;
25; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3.
TNER-CYS 4.
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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BY SIMILARII
BY SIMILARII
BY SIMILARII
                                                                                                                                                                     CYTOPLASMIC (POTENTIAL). 4 X TNFR-CYS.
                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                  RECEPTOR
                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                      POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                               REGION
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Best Local Similarity
Thes 54; Conserv
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P259443;
01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECUR
                                                                   CHAIN
DOMAIN
REPEAT
                                                                                                                              EMBL; M17433; ; NOT_ANNOTATED_CDS.
EMBL; A23727; E199408; -
PIR, B43692, B43692.
HSSP; P19438; JTNR.
                                                                                                                                                                   MEDLINE; 91207415.

SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C., MCRADDEN G., GOODWIN R.G.;

BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).

-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TREACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 87321103.
UPTON C., DELANGE A.M., M
VIROLOGY 160:20-30(1987).
                                                                                                                                                                                                                                                                                                                                   SHOPE FIBROMA VIRUS (STRAIN KASZA) VIRIDAE; DS-DNA ENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                         VIRIDAE: DS-DNA
LEPORIPOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144
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                                                                                                   IGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eevapctsdrkaecrcqpgmscvyldnecvhceeexlvlcqpgteaevtdeimdtdvncv 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE-LQY 92
                PS00652; TNFR_NGFR.
(; GLYCOPROTEIN; REPERINGEN)
17 16
17 325
17 325
27 62
27 62
27 62
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                                                                                                            REPEAT; SIGNAL
                                                                                                                                                                                                                                                                                  MCFADDEN
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BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                            PROTENTIAL.
PROTEIN 12.
4 X TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLEIE--FCLKHR-S-CPPGFGV-VQAGTPERNTVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 265; DB 9;
Pred. No. 3.52e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
3C5DD121
                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                  <u>ه</u>.
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                                                                                                                                                                                                                                                                                                                                   (SFV).
POXVIRIDAE; CHORDOPOXVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 415
                                                                                                                                                                                                                                                                                                                                                                 (PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Query Match
Best Local S
Matches 5
   REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                              DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CROWE P.D., VAN AR
                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                HSSP; P19999; 1CLG.
PROSITE; PS00652; T
RECEPTOR; TRANSMEMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CROWE P.D., VAN ARSDALE T.L., WALTER B.N., WARE C.F., EHRENFELS B., BROWNING J.L., DIN W.S., GOODWIN R.G., SCIENCE 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAENS M., CHAFFANET M., C
GENOMICS 16:214-218(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LIVER;
MEDLINE; 93252381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           мім; 600979; -

    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
    -!- SIMILARITY: CONTAINS A LA-NGFR/TMFR-TYPE CYSTEINE-RICH

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155
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                                                                                                                                                                                                                                                                                                                                                       IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMUNE DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sptercgtsfnyisvgfnlypvnetscttt-aghneviktkeftvtl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hdrvcncstgnycllkgqngcricapqtkcpagygvs-ghtragdtlcekcpphtysdsl
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                                                                                                                                                                                                                                                                                                                                                                                                                                         .04270; G339762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Similarity
51; Conser
                                                                                                                                                                                                                                                                                                                                                                      PS00652; TNFR_NGFR.
TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
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llarity 30.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 260; DB 10; 1
Pred. No. 3.98e-31;
31; Mismatches 77;
THER-CYS.
THER-CYS 1.
THER-CYS 2.
THER-CYS 3.
THER-CYS 3.
THER-CYS 4.
BY SIMILARITY
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                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                    POTENTIAL.
                Y SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEN
                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BERGHE
                                                                                                                                                                                                                                                                                                                                       RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                      SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MARYNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.A.;
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Best Local Similarity 32.3%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Matches
   TNR1_MOUSE
P25118;
01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;
FEBS LETT. 319:80-83(1993).
-!- SIMILARIIY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
EMBL; X691198; G457087; -.
EMBL; X67117; G516449; -.
ENBL; X67117; G516449; -.
ENBL; X67187 D36858.
D1R; D36858, D36858.
PIR; S35987; S35987.
PIR; S46888, S46888.
HSSP; P19438; LTNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UC22_VARV STANDARD; PRT; 3
P34015; P34015
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UP
01-JUN-1994 (REL. 29, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P1
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIOLA VIRUS.
VIRIDAE; DS-DNA
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-INDIA-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93202281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORTHOPOXVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN C22/B28 HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145
                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 ckaghfqntsspsarcqphtrcenqglveaapgtaqsdttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111
                                                                                                                                             159 shtvssadkc 168
|: || |
                                                                                                                                                                                                                 100 cntthnricecspgyycllkgssgckacvsqtkcgigygvs-ghtsvgdvicspcgfgty 158
                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                    40 hnlcclscppgtyasrlcdsktntqctpcgsgtftsrnnhlpaclscngrcnsnqvetrs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYVKQECNRTHNRVCECKEGRY-----LEIEFCLKHRSCPPGFGV-VQAGTPERNTVCKR
                                                                                                                                                                                                                                                                HQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eeiap-ctskrktqcrcqpqmfcaawalecthcellsdcppqteaelkdevgkgnnhcvp 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKEL
                                                                                                                         SNETSSKAPC
                                                                                                                                                                                             CNRTHNRVCECKEGRY -- LE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        31
31
67
349 AA;
   (REL.
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                      STANDARD;
                                                                                                                           160
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38189
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801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46709 MW;
   CREATED)
LAST SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                · IE - - FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFF
                                                                                                                                                                                                                                                                                                                                 Score 230; DB 10;
Pred. No. 6.59e-25;
19; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 260; DB 9;
Pred. No. 3.98e-31;
23; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                         2 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
203B82DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                          50D0B435 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ON UPDATE)
     UPDATE)
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P SEQUENCE FROM N.A.

N. MEDILINE; 93156721,

A. ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;

A. ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;

A. MOL. IMMUNOL. 30:165-175(1993).

C. -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.

C. -!- FUNCTION: RECEPTOR FOR TYPE I MEMBRANE PROTEIN.

C. -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -!- SUBCELLULAR LOCATION: A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONE MEMBL; M60468; G199826; --

NR EMBL; M60468; G199826; --

EMBL; M59377; G202097; --

DR EMBL; M59377; G202097; --

EMBL; M59377; G202102; --

EMBL; M56546; G202102; --

EMBL; M76655; G202102; JOINED.

EMBL; M76655; G202102; JOINED.
   REPEAT
REPEAT
REPEAT
REPEAT
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DISULFID
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                                                                                                                                                                                                             DOMAIN
TRANSMEM
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SEQUENCE FROM N.A.
MEDLINE; 91246168.
MEDLINE; 91246168.
GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
COPELAND N.G., JENKINS N.A., SMITH C.A.;
COPELAND N.G., JENKINS N.A., SMITH C.A.;
CELL. BIOL. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; TNFR_NGFR.
PROSITE; PS50017; DEATH_DOMAIN
                                                                                                                                                                                                                                                                                                                                                              PIR; S16677;
PIR; S19021;
                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A38634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., GRAY P.W., FELDMANN M., FOXWELL B.M.J.; EUR. J. IMMUNOL. 21:1649-1656(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A., LEE
WONG G.H., CHEN E.Y., GOEDDEL
PROC. NATL. ACAD. SCI. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (REL. 34, TUMOR NECROSIS FACTOR TNFR1 OR TNFR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 94245292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92039815.
ROTHE J.G., BROCKHAUS M., GENTZ
IMMUNOGENETICS 34:338-340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 91285014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMUNOGENETICS 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                            A38634; GQMST1.
S16677; S16677.
S19021; S19021.
; P19438; lTNR.
                                                                                                                                                                                                                                                                                         TRANSMEMBRANE;
     LAST ANNOTATION UPDATE;
RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                                                                                                                                                     GLYCOPROTEIN; REPEAT; SIGNAL.
TNFR-CYS 1.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                        CYTOPLASMIC (POTENTIAL). 4 X TNFR-CYS.
                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A., BENNETT G.L., R
D.V.;
88:2830-2834(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KISSONERGHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RICE G.C.,
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Best Local s
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P22934:
01-AUG-1991 (REL. 19, C
01-MAR-1992 (REL. 21, L
01-NOV-1995 (REL. 32, L
TUMOR NECROSIS FACTOR R
TNER1 OR TNER-1.
                                                                                                                                                                                                                                                                                                               REPEAT
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CONFLICT
SEQUENCE
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REPEAT
                                                                                                                                                                                                                                                                                  RECEPTOR;
SIGNAL
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EUKARYOTA; METAZOA; CHOF
EUTHERIA; RODENTIA.
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNR1_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 RCPDGFFSNETSSKA-P-CRKHTNC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 -chagfflresecvpcshckkneec 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yvhsknnsicctkchkgtylvsdcpspgrdtvcrecekgtftasgnylrgclscktcrke 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQYVK-QECNRTHNRVCECKEG---RYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 7.7%;
Similarity 33.1%;
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91090841.
                                                                                                                                                                                                                                                                                                     TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                                                                                                                                                                   GLYCOPROTEIN; REPEAT; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥.
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Pred. No. 4.45e-23
21; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
DEATH DOMAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                 4 X INFR-CYS.

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.
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POTENTIAL.
R -> G (IN
                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                               TNFR-CYS 4
                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> G (IN REF. 6).
4B6EEC09 CRC32;
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CHAIN SIGNAL HSSP;

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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGFR_CHICK P18519;
                                                                                                                                                       PIR; JN0006; JN0006.
PIR; A60504; A60504.
PROSITE; PS000652; TUFR_NGFR.
PROSITE; PS50017; DEATH_DOMAIN.
RECEPTOR; NEUROGENESIS; TRANSMEMBRANE;
PHOSPHORYLATION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEURON
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE: 90166579.

LARGE T.H., WESKAMP G.,

SHOOTER E.M., REICHARDT

NEURON 2:1123-1134(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALLUS GALLUS (CHICK
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 21-416 FROM N.A. MEDLINE; 90152140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRE
                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-BRAIN;
                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GP80-LNGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ω</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-OYVKQECNRTHNRVCECK--E-GRYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yahpknnsicctkchkgtylvsdcpspgqetvcevcdkgtftasqnhvrqclscktcrke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCPDGFF-S-NETSSKAPCRKHTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -chagfflsgnectpcshckkngec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 7.7%;
Similarity 33.8%;
49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
127
146
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201
461 PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
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50969
    19
416
239
261
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416
181
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW;
NGF RECEPTOR.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X THER-CYS 1.
THER-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 220; DB 9;
Pred. No. 7.09e-23;
22; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RADEKE
                                                                                                                                                                                  GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRECURSOR (NGF
                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              м.ј.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVES; NEOGNATHAE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
TRESULT TO DEPART OF THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
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Best Local s
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGFR_HUMAN
P08138;
01-AUG-1988 (
01-AUG-1988 (
01-NOV-1995 (
LOW-AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMANIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GP80-LNGFR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 APCRKHINCSVFGLLLTQKGNATHDNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
45; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%;
larity 30.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
2181
2181
2181
2181
356
356
396
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHORDATA;
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Score 215; DB 6;
Pred. No. 7.20e-22;
27; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                            DEATH DOMAIN.
BY SIMILARITY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 3.
TNFR-CYS 4.
SER/THR-RICH.
DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                    4D3F086A
                                                                                                                                                                                                                                                                                                                                                                                 REF.
                                                                                                                                                                                                                                                                                                                                                                            Length 416
                                                                                                                 Indels
                                                                                                            6
                                                                                                      Gaps
93
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100 THNRVCECKEGRYL-EIE-FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSK 157 dpclpcticeenevmvke-ctatsdaec sddavcrcaygyfqdelsgsckecsicevgfglmfpcrdsqdtvceecpegtfsdeanfv 153 180 99 σ,

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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE
-!- PTM: N- AND O-GLYCOSYLATED AND IS PHO
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-T
EMBL; M14764; G189205; -
PIR: A25218; GOHUN.
HSSP; P19438; 1TNR.
MIM; 162010; -
PROSITE; PS00052; TNER_NGFR.
PROSITE; PS00052; TNER_NGFR.
PROSITE; PS00017: DEATH_DOMAIN.
RECEPPOR; NEUROGENESIS; TRANSMEMBRANE; GL
PHOSPHORYLATION; SIGNAL.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 87051725.
JOHNSON D., LANAHAN A., BUCK C.R., SEHGAL
BOTHWELL M., CHAO M.;
CELL 47:545-554(1986).
-1- FUNCTION; LOW AFFINITY RECEPTOR WHICH
                                                                                                                                                                                                                                           NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 08, CREATED)
(REL. 08, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
V NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                          A LA-NGFR/TNFR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                MEMBRANE PROTEIN.
ND IS PHOSPHORYLATED ON SERINE
                                                                                                                                                                                                                                                                                                                                                                        SEHGAL A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427
                        GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ž
                                                                                                                                                                                                                                                                                                          CAN
                                                                                                                                                                            CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                        MORGAN
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                                                                                                                                                                                                                                                             THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                       TO
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                                                                                                                                                                                                                                                                                                          NGF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
METSIS M., TIMMUSK T., ALLIKMETS R.
GENE 121:247-254(1992).

-!- FUNCTION: LOW AFFINITY RECEPTOR

-!- SUBUNIT: NGF RECEPTOR CAN FORM
BOND FORMATION.

-!- SUBCELLULAR LOCATION: TYPE I MI

-!- SUBCELLULAR LOCATION: TYPE I MI

-!- SUBCELLULAR LOCATION: TYPE I MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DISULFID
                                                                                                                                                                                                                                                             NGFR_RAT
P07174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                      01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR
                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 87115859.
RADEKE M.J., MISKO T.P.,
RATURE 325:593-597(1987).
                                                                                                                                                                               RATTUS NORVEGICUS (I EUKARYOTA; METAZOA;
                                                                                                 SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                     EUTHERIA; RODENTIA
                                                                                                                                                                                                             (GP80-LNGFR).
                                                                                                                                                                                                                                                                                                               158
                                                                                                                                                                                                                                                                                                                                   162
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                                                                                                                                                                                                                                                                                                                                                                                                      44 ckacnlgegvagpcgan-qtvcepcldsvtfsdvvsatepckpcte-cvglqsmsapcve 101
                                                                                                                                                                                                                                                                                                                              dpclpctvc 170
                                                                                                                                                                                                                                                                                                                                                                 APCRKHINC 166
                                                                                                                                                                                                                                                                                                                                                     THURVCECKEGRYL-EI-EFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSK 157
                                                                                                                                                                                                                                                                                                                                                                                            CDKCPPGTYLKQHCTAKWKTVCAPCPDHY-YTDSWHTSDECLYCSPVCKELQYVKQECNR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                 h 7.4%;
Similarity 34.9%;
45; Conservative
                                                                            93077038.
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A
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RAT)
                                                                                                                                                                                CHORDATA; VERTEBRATA;
                                                                                                                               HSU C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                              CAN FORM A HOMODIMER THROUGH DISULFIDE
                                                   RECEPTOR WHICH CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.81e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 213; DB 6;
Pred. No. 1.81e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SER/THR-RICH.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGF RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATH DOMAIN.
Y SIMILARITY
  I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EE2924BD CRC32;
                                                                    .
К
                                                                                                                                HERZENBERG
                                                                                                                                                                                                                                                                       425
                                                                    SAARMA M.,
   PHOSPHORYLATED
                                                                                                                                                                                 TETRAPODA; MAMMALIA
                                                                                                                               L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                  BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                     PERSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                               SHOOTER E.
                                                                                                                                                                                                                      (NGF RECEPTOR)
   õ
                                                   NGF,
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    CCCEPRENCOCS CEETTE
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Best Local S
Matches 4
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DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                         APT1 OR FAS.
BOS TAURUS (1
EUKARYOTA; MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
REPEAT
                                                                                                                               PASA_BOVIN STANDARD; PRT; 323 AA. p51867; 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE) FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING)
SEQUENCE FROM N.A.

MEDLINE; 96226401.

YOO J., STONE R.T., BEATTIE C.W.;

YOO J., STONE R.T., BEATTIE C.W.;

DNA CELL BIOL. 15:227-234(1996).

-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MI

CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00652; TNFR_NGFR.
PROSITE: PS50017; DEATH_DOMAIN.
RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION EMBL; X05137; 656756; -. ROT_ANNOTATED_CDS.
PIR; A26431; A26431.
HSSP; P19438; 1TNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                SUTHERIA; ARTIODACTYLA
                                                                                                                                                                                                                                                                                                          103 addavcrcaygyyqdeetghceacsvcevgsglvfscqdkqntvceecpegtysdeanhv 162
                                                                                                                                                                                                                                           158 APCRKHINC 166
                                                                                                                                                                                                                                                                 163 dpclpctvc 171
                                                                                                                                                                                                                                                                                       100 THNRVCECKEGRYLEIE--FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSK 157
                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                           45
                                                                                                                                                                                                                                                                                                                                                 CDKCPPGTYLKQHCTAKWKTVCAPCPDHY-YTDSWHTSDECLYCSPVCKELQYVKQECNR
                                                                                                                            ANTIGEN) (CD95).
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
43; Conser
                                                                                         (BOVINE).
                                                                                                                                                                                                                                                                                                                                                                                7.2%;
larity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
273
425
190
108
148
148
                                                                                          CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                              45432
                                                                                                                                                                                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                Score 207;
Pred. No. 2.
21; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 X TNFR-CYS.1.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
SER/THR-RICH.
DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGF RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                          VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                              CRC32;
                                                                                          TETRAPODA; MAMMALIA;
                                                                                                                                       SURFACE ANTIGEN FAS)
                                                                                                                                                                                                                                                                                                                                                                                                      Length 425
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                 5
              MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Search completed: Wed Aug 20 09:55:23 1997 Job time : 76 secs.
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                                                                                             В
                                                                                                                                                                                       Ouery Match 6.6%;
st Local Similarity 35.7%;
atches 40; Conservative
                                                                                                                                                                                                                                                     REPEAT
REPEAT
REPEAT
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

EMBL; U34794; G1262193; -.
                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                              NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                 APOPTOSIS; RECEPTOR;
                                                                                                                         36445 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
6 POTENTIAL.
                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
3 X THER-CYS.
TIFR-CYS 1.
THER-CYS 2.
THER-CYS 3.
THER-CYS 3.
DEATH DOMAIN.
DA5A2A59 CRC32;
                                                                                                                                                                                       Score 188; DB 3; Length 323;
Pred. No. 1.51e-16;
17; Mismatches 49; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                FASL RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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